

1653

1600

RAW SEQUENCE LISTING

PATENT APPLICATION: US/09/635,949

DATE: 11/28/2001 P.S.
TIME: 10:30:22

Input Set : A:\Cur59p21.app

Output Set: N:\CRF3\11212001\I635949.raw

ENTERED

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3 <110> APPLICANT: SHIMKETS, RICHARD A
4   FERNANDES, ELMA
6 <120> TITLE OF INVENTION: POLYNUCLEOTIDES AND POLYPEPTIDES ENCODED THEREBY
8 <130> FILE REFERENCE: 15966-559
10 <140> CURRENT APPLICATION NUMBER: 09/635,949
11 <141> CURRENT FILING DATE: 2000-08-10
13 <150> PRIOR APPLICATION NUMBER: USSN 60/148,433
14 <151> PRIOR FILING DATE: 1999-08-11
16 <160> NUMBER OF SEQ ID NOS: 110
18 <170> SOFTWARE: PatentIn Ver. 2.1
20 <210> SEQ ID NO: 1
21 <211> LENGTH: 1867
22 <212> TYPE: DNA
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34 ggcaagg atg gag ctg ggt tgc tgg acg cag ttg ggg ctc act ttt ctt 169
35   Met Glu Leu Gly Cys Trp Thr Gln Leu Gly Leu Thr Phe Leu
36       1           5           10
38 cag ctc ctt ctc atc tgc tcc ttg cca aga gag tac aca gtc att aat 217
39 Gln Leu Leu Leu Ile Ser Leu Pro Arg Glu Tyr Thr Val Ile Asn
40 15           20           25           30
42 gaa gcc tgc cct gga gca gag tgg aat atc atg tgt cgg gag tgc tgt 265
43 Glu Ala Cys Pro Gly Ala Glu Trp Asn Ile Met Cys Arg Glu Cys Cys
44           35           40           45
46 gaa tat gat cag att gag tgc gtc tgc ccc gga aag agg gaa gtc gtg 313
47 Glu Tyr Asp Gln Ile Glu Cys Val Cys Pro Gly Lys Arg Glu Val Val
48           50           55           60
50 ggt tat acc atc cct tgc tgc agg aat gag gag aat gag tgt gac tcc 361
51 Gly Tyr Thr Ile Pro Cys Cys Arg Asn Glu Glu Asn Glu Cys Asp Ser
52           65           70           75
54 tgc ctg atc cac cca ggt tgt acc atc ttt gaa aac tgc aag agc tgc 409
55 Cys Leu Ile His Pro Gly Cys Thr Ile Phe Glu Asn Cys Lys Ser Cys
56           80           85           90
58 cga aat ggc tca tgg ggg ggt acc ttg gat gac ttc tat gtg aag ggg 457
59 Arg Asn Gly Ser Trp Gly Gly Thr Leu Asp Asp Phe Tyr Val Lys Gly
60 95           100           105           110
62 ttc tac tgt gca gag tgc cga gca ggc tgg tac gga gga gac tgc atg 505
63 Phe Tyr Cys Ala Glu Cys Arg Ala Gly Trp Tyr Gly Gly Asp Cys Met
64           115           120           125
66 cga tgt ggc cag gtt ctg cga gcc cca aag ggt cag att ttg ttg gaa 553
67 Arg Cys Gly Gln Val Leu Arg Ala Pro Lys Gly Gln Ile Leu Leu Glu
68           130           135           140

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70 agc tat ccc cta aat gct cac tgt gaa tgg acc att cat gct aaa cct 601
71 Ser Tyr Pro Leu Asn Ala His Cys Glu Trp Thr Ile His Ala Lys Pro
72      145      150      155
74 ggg ttt gtc atc caa cta aga ttt gtc atg ttg agc ctg gag ttt gac 649
75 Gly Phe Val Ile Gln Leu Arg Phe Val Met Leu Ser Leu Glu Phe Asp
76      160      165      170
78 tac atg tgc cag tat gac tat gtt gag gtt cgt gat gga gac aac cgc 697
79 Tyr Met Cys Gln Tyr Asp Tyr Val Glu Val Arg Asp Gly Asp Asn Arg
80 175      180      185      190
82 gat ggc cag atc atc aag cgt gtc tgt ggc aac gag cgg cca gct cct 745
83 Asp Gly Gln Ile Ile Lys Arg Val Cys Gly Asn Glu Arg Pro Ala Pro
84      195      200      205
86 atc cag agc ata gga tcc tca ctc cac gtc ctc ttc cac tcc gat ggc 793
87 Ile Gln Ser Ile Gly Ser Ser Leu His Val Leu Phe His Ser Asp Gly
88      210      215      220
90 tcc aag aat ttt gac ggt ttc cat gcc att tat gag gag atc aca gca 841
91 Ser Lys Asn Phe Asp Gly Phe His Ala Ile Tyr Glu Glu Ile Thr Ala
92      225      230      235
94 tgc tcc tca tcc cct tgt ttc cat gac ggc acg tgc gtc ctt gac aag 889
95 Cys Ser Ser Ser Pro Cys Phe His Asp Gly Thr Cys Val Leu Asp Lys
96      240      245      250
98 gct gga tct tac aag tgt gcc tgc ttg gca ggc tat act ggg cag cgc 937
99 Ala Gly Ser Tyr Lys Cys Ala Cys Leu Ala Gly Tyr Thr Gly Gln Arg
100 255      260      265      270
102 tgt gaa aat ctc ctt gaa gaa aga aac tgc tca gac cct ggg ggc cca 985
103 Cys Glu Asn Leu Leu Glu Glu Arg Asn Cys Ser Asp Pro Gly Gly Pro
104      275      280      285
106 gtc aat ggg tac cag aaa ata aca ggg ggc cct ggg ctt atc aac gga 1033
107 Val Asn Gly Tyr Gln Lys Ile Thr Gly Gly Pro Gly Leu Ile Asn Gly
108      290      295      300
110 cgc cat gct aaa att ggc acc gtg gtg tct ttc ttt tgt aac aac tcc 1081
111 Arg His Ala Lys Ile Gly Thr Val Val Ser Phe Phe Cys Asn Asn Ser
112      305      310      315
114 tat gtt ctt agt ggc aat gag aaa aga act tgc cag cag aat gga gag 1129
115 Tyr Val Leu Ser Gly Asn Glu Lys Arg Thr Cys Gln Gln Asn Gly Glu
116      320      325      330
118 tgg tca ggg aaa cag ccc atc tgc ata aaa gcc tgc cga gaa cca aag 1177
119 Trp Ser Gly Lys Gln Pro Ile Cys Ile Lys Ala Cys Arg Glu Pro Lys
120 335      340      345      350
122 att tca gac ctg gtg aga agg aga gtt ctt ccg atg cag gtt cag tca 1225
123 Ile Ser Asp Leu Val Arg Arg Arg Val Leu Pro Met Gln Val Gln Ser
124      355      360      365
126 agg gag aca cca tta cac cag cta tac tca gcg gcc ttc agc aag cag 1273
127 Arg Glu Thr Pro Leu His Gln Leu Tyr Ser Ala Ala Phe Ser Lys Gln
128      370      375      380
130 aaa ctg cag agt gcc cct acc aag aag cca gcc ctt ccc ttt gga gat 1321
131 Lys Leu Gln Ser Ala Pro Thr Lys Lys Pro Ala Leu Pro Phe Gly Asp
132      385      390      395
134 ctg ccc atg gga tac caa cat ctg cat acc cag ctc cag tat gag tgc 1369

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135 Leu Pro Met Gly Tyr Gln His Leu His Thr Gln Leu Gln Tyr Glu Cys
136      400                      405                      410
138 atc tca ccc ttc tac cgc cgc ctg ggc agc agc agg agg aca tgt ctg      1417
139 Ile Ser Pro Phe Tyr Arg Arg Leu Gly Ser Ser Arg Arg Thr Cys Leu
140 415                      420                      425                      430
142 agg act ggg aag tgg agt ggg cgg gca cca tcc tgc atc cct atc tgc      1465
143 Arg Thr Gly Lys Trp Ser Gly Arg Ala Pro Ser Cys Ile Pro Ile Cys
144                      435                      440                      445
146 ggg aaa att gag aac atc act gct cca aag acc caa ggg ttg cgc tgg      1513
147 Gly Lys Ile Glu Asn Ile Thr Ala Pro Lys Thr Gln Gly Leu Arg Trp
148                      450                      455                      460
150 ccg tgg cag gca gcc atc tac agg agg acc agc ggg gtg cat gac ggc      1561
151 Pro Trp Gln Ala Ala Ile Tyr Arg Arg Thr Ser Gly Val His Asp Gly
152                      465                      470                      475
154 agc cta cac aag gga gcg tgg ttc cta gtc tgc agc ggt gcc ctg gtg      1609
155 Ser Leu His Lys Gly Ala Trp Phe Leu Val Cys Ser Gly Ala Leu Val
156      480                      485                      490
158 aat gag cgc act gtg gtg gtg gct gcc cac tgt gtt act gac ctg ggg      1657
159 Asn Glu Arg Thr Val Val Val Ala Ala His Cys Val Thr Asp Leu Gly
160 495                      500                      505                      510
162 aag gtc acc atg atc aag aca gca gac ctg aaa gtt gtt ttg ggg aaa      1705
163 Lys Val Thr Met Ile Lys Thr Ala Asp Leu Lys Val Val Leu Gly Lys
164                      515                      520                      525
166 ttc tac cgg gat gat gac cgg gat gag aag acc atc cag agc cta cag      1753
167 Phe Tyr Arg Asp Asp Asp Arg Asp Glu Lys Thr Ile Gln Ser Leu Gln
168                      530                      535                      540
170 att tct gct atc att ctg cat ccc aac tat gac ccc atc ctt gct ttg      1801
171 Ile Ser Ala Ile Ile Leu His Pro Asn Tyr Asp Pro Ile Leu Ala Leu
172                      545                      550                      555
174 atg ctt gac atc gcc atc ctg aac tcc tagacaaggc ccgtatcagc      1848
175 Met Leu Asp Ile Ala Ile Leu Asn Ser
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181 <210> SEQ ID NO: 2
182 <211> LENGTH: 567
183 <212> TYPE: PRT
184 <213> ORGANISM: Homo sapiens
186 <400> SEQUENCE: 2
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191      20      25      30
193 Cys Pro Gly Ala Glu Trp Asn Ile Met Cys Arg Glu Cys Cys Glu Tyr
194      35      40      45
196 Asp Gln Ile Glu Cys Val Cys Pro Gly Lys Arg Glu Val Val Gly Tyr
197      50      55      60
199 Thr Ile Pro Cys Cys Arg Asn Glu Glu Asn Glu Cys Asp Ser Cys Leu
200 65      70      75      80
202 Ile His Pro Gly Cys Thr Ile Phe Glu Asn Cys Lys Ser Cys Arg Asn

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Input Set : A:\Cur59p21.app
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203				85				90				95				
205	Gly	Ser	Trp	Gly	Gly	Thr	Leu	Asp	Asp	Phe	Tyr	Val	Lys	Gly	Phe	Tyr
206				100					105					110		
208	Cys	Ala	Glu	Cys	Arg	Ala	Gly	Trp	Tyr	Gly	Gly	Asp	Cys	Met	Arg	Cys
209				115					120					125		
211	Gly	Gln	Val	Leu	Arg	Ala	Pro	Lys	Gly	Gln	Ile	Leu	Leu	Glu	Ser	Tyr
212				130					135					140		
214	Pro	Leu	Asn	Ala	His	Cys	Glu	Trp	Thr	Ile	His	Ala	Lys	Pro	Gly	Phe
215	145						150					155				160
217	Val	Ile	Gln	Leu	Arg	Phe	Val	Met	Leu	Ser	Leu	Glu	Phe	Asp	Tyr	Met
218					165				170						175	
220	Cys	Gln	Tyr	Asp	Tyr	Val	Glu	Val	Arg	Asp	Gly	Asp	Asn	Arg	Asp	Gly
221				180					185					190		
223	Gln	Ile	Ile	Lys	Arg	Val	Cys	Gly	Asn	Glu	Arg	Pro	Ala	Pro	Ile	Gln
224				195					200					205		
226	Ser	Ile	Gly	Ser	Ser	Leu	His	Val	Leu	Phe	His	Ser	Asp	Gly	Ser	Lys
227				210				215					220			
229	Asn	Phe	Asp	Gly	Phe	His	Ala	Ile	Tyr	Glu	Glu	Ile	Thr	Ala	Cys	Ser
230	225					230					235					240
232	Ser	Ser	Pro	Cys	Phe	His	Asp	Gly	Thr	Cys	Val	Leu	Asp	Lys	Ala	Gly
233					245					250					255	
235	Ser	Tyr	Lys	Cys	Ala	Cys	Leu	Ala	Gly	Tyr	Thr	Gly	Gln	Arg	Cys	Glu
236				260					265					270		
238	Asn	Leu	Leu	Glu	Glu	Arg	Asn	Cys	Ser	Asp	Pro	Gly	Gly	Pro	Val	Asn
239				275					280					285		
241	Gly	Tyr	Gln	Lys	Ile	Thr	Gly	Gly	Pro	Gly	Leu	Ile	Asn	Gly	Arg	His
242				290				295					300			
244	Ala	Lys	Ile	Gly	Thr	Val	Val	Ser	Phe	Phe	Cys	Asn	Asn	Ser	Tyr	Val
245	305					310					315					320
247	Leu	Ser	Gly	Asn	Glu	Lys	Arg	Thr	Cys	Gln	Gln	Asn	Gly	Glu	Trp	Ser
248					325					330					335	
250	Gly	Lys	Gln	Pro	Ile	Cys	Ile	Lys	Ala	Cys	Arg	Glu	Pro	Lys	Ile	Ser
251				340					345					350		
253	Asp	Leu	Val	Arg	Arg	Arg	Val	Leu	Pro	Met	Gln	Val	Gln	Ser	Arg	Glu
254				355					360					365		
256	Thr	Pro	Leu	His	Gln	Leu	Tyr	Ser	Ala	Ala	Phe	Ser	Lys	Gln	Lys	Leu
257				370				375					380			
259	Gln	Ser	Ala	Pro	Thr	Lys	Lys	Pro	Ala	Leu	Pro	Phe	Gly	Asp	Leu	Pro
260	385					390					395					400
262	Met	Gly	Tyr	Gln	His	Leu	His	Thr	Gln	Leu	Gln	Tyr	Glu	Cys	Ile	Ser
263					405					410					415	
265	Pro	Phe	Tyr	Arg	Arg	Leu	Gly	Ser	Ser	Arg	Arg	Thr	Cys	Leu	Arg	Thr
266					420					425				430		
268	Gly	Lys	Trp	Ser	Gly	Arg	Ala	Pro	Ser	Cys	Ile	Pro	Ile	Cys	Gly	Lys
269				435					440					445		
271	Ile	Glu	Asn	Ile	Thr	Ala	Pro	Lys	Thr	Gln	Gly	Leu	Arg	Trp	Pro	Trp
272				450				455				460				
274	Gln	Ala	Ala	Ile	Tyr	Arg	Arg	Thr	Ser	Gly	Val	His	Asp	Gly	Ser	Leu
275	465					470					475					480

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277 His Lys Gly Ala Trp Phe Leu Val Cys Ser Gly Ala Leu Val Asn Glu
278                               485                490                495
280 Arg Thr Val Val Val Ala Ala His Cys Val Thr Asp Leu Gly Lys Val
281                               500                505                510
283 Thr Met Ile Lys Thr Ala Asp Leu Lys Val Val Leu Gly Lys Phe Tyr
284                               515                520                525
286 Arg Asp Asp Asp Arg Asp Glu Lys Thr Ile Gln Ser Leu Gln Ile Ser
287                               530                535                540
289 Ala Ile Ile Leu His Pro Asn Tyr Asp Pro Ile Leu Ala Leu Met Leu
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293                               565
297 <210> SEQ ID NO: 3
298 <211> LENGTH: 2306
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300 <213> ORGANISM: Homo sapiens
302 <220> FEATURE:
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311 ggcaagg atg gag ctg ggt tgc tgg acg cag ttg ggg ctc act ttt ctt 169
312 Met Glu Leu Gly Cys Trp Thr Gln Leu Gly Leu Thr Phe Leu
313 1 5 10
315 cag ctc ctt ctc atc tcg tcc ttg cca aga gag tac aca gtc att aat 217
316 Gln Leu Leu Leu Ile Ser Ser Leu Pro Arg Glu Tyr Thr Val Ile Asn
317 15 20 25 30
319 gaa gcc tgc cct gga gca gag tgg aat atc atg tgt cgg gag tgc tgt 265
320 Glu Ala Cys Pro Gly Ala Glu Trp Asn Ile Met Cys Arg Glu Cys Cys
321 35 40 45
323 gaa tat gat cag att gag tgc gtc tgc ccc gga aag agg gaa gtc gtg 313
324 Glu Tyr Asp Gln Ile Glu Cys Val Cys Pro Gly Lys Arg Glu Val Val
325 50 55 60
327 ggt tat acc atc cct tgc tgc agg aat gag gag aat gag tgt gac tcc 361
328 Gly Tyr Thr Ile Pro Cys Cys Arg Asn Glu Glu Asn Glu Cys Asp Ser
329 65 70 75
331 tgc ctg atc cac cca ggt tgt acc atc ttt gaa aac tgc aag agc tgc 409
332 Cys Leu Ile His Pro Gly Cys Thr Ile Phe Glu Asn Cys Lys Ser Cys
333 80 85 90
335 cga aat ggc tca tgg ggg ggt acc ttg gat gac ttc tat gtg aag ggg 457
336 Arg Asn Gly Ser Trp Gly Gly Thr Leu Asp Asp Phe Tyr Val Lys Gly
337 95 100 105 110
339 ttc tac tgt gca gag tgc cga gca ggc tgg tac gga gga gac tgc atg 505
340 Phe Tyr Cys Ala Glu Cys Arg Ala Gly Trp Tyr Gly Gly Asp Cys Met
341 115 120 125
343 cga tgt ggc cag gtt ctg cga gcc cca aag ggt cag att ttg ttg gaa 553
344 Arg Cys Gly Gln Val Leu Arg Ala Pro Lys Gly Gln Ile Leu Leu Glu
345 130 135 140

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Use of n and / or Xaa has been detected in the
Sequence Listing. Review the Sequence Listing
to ensure a corresponding explanation is present
in the <220> to <223> fields of each sequence
using n or Xaa.

VERIFICATION SUMMARY

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Input Set : A:\Cur59p21.app

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L:2128 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:15
L:2635 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:17
L:2909 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:19
L:3447 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:23
L:3971 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:27